

Laboratory work nr. 1

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As a small sidenote. A couple of packages used are different from the laboratory task. As a second sidenote. import * allows to use sub-packages as well.

```
In [64]: from sklearn import *
import numpy as np
import seaborn as sb
from sklearn.decomposition import PCA
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
import pandas as pd
from sklearn.neighbors import KNeighborsClassifier, NeighborhoodComponentsAnalysis
from sklearn.pipeline import make_pipeline
from sklearn.preprocessing import StandardScaler
from keras.datasets import mnist
from keras.models import Sequential
from keras.layers import Dense
from keras.layers import Dropout
from keras.utils import np_utils

In [31]: # A.3
iris_dataset = datasets.load_iris()
```

```
In [32]: # A.4 print them all
print(f'Number fo data: {n} % len(iris_dataset.data)')
print(f'Names of variables: {s} % iris_dataset.feature_names')
p=6.812001-0.676classes: {s} % iris_dataset.target_names)

Number fo data: 150
Names of variables: ['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)', 'petal width (cm)']
Names of classes: ['setosa' 'versicolor' 'virginica']

In [33]: # A.5
names_of_classes = iris_dataset.target_names
for data, target in zip(iris_dataset.data, iris_dataset.target):
    print(f'Object {n} => Class {s} % (data, names_of_classes[target])')

Object [5.1 3.5 1.4 0.2] ==> Class setosa
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```

```
In [34]: # B.1
X = np.asarray([[1, -1, 2],
                [2, 0, 0],
                [0, 1, -1]])

# B.2
print(f'matrix: {s} % X')
print(f'mean: {s} % X.mean())
print(f'variance: {s} % X.var())

matrix: [[ 1 -1  2]
 [ 2  0  0]
 [ 0  1 -1]]
mean: 0.4444444444444444
variance: 1.1358024691358024
```

```
In [35]: # B.3
X = preprocessing.scale(X)
# WELL, it changed variables to values closer to -1, 0 and 1 instead of 2, this should improve the results of PCA
```

```
In [36]: # B.4
print('NEW')
print(f'matrix: {s} % X')
print(f'mean: {s} % X.mean())
print(f'variance: {s} % X.var())
# Conclusion: they changed. Mean is now very low, closer to 0 instead of being closer to 0.5
# Variance didn't change much, well, no real improvement.

NEW
matrix: [[ 0.          -1.22474487  1.33630621]
 [ 1.22474487   0.         -0.26726124]
 [ -1.22474487  1.22474487  -1.06904491]]
mean: 0.493432455389598446-17
variance: 1.0
```

```
In [37]: # C.1
X2 = np.asarray([[1, -1, 2],
                 [2, 0, 0],
                 [0, 1, -1]])

# C.2
print(f'Mean of vars X2: {s} % X2.mean())

Mean of vars X2: 0.4444444444444444
```

```
In [38]: # C.3
scaler = preprocessing.MinMaxScaler()
transformed_data = scaler.fit_transform(X2)
print('Transformed')
print(f'matrix: {s} % transformed_data')
print(f'mean: {s} % transformed_data.mean())
print(f'variance: {s} % transformed_data.var())
# Although mean returned to previous values (and we don't really care about it because it is all about the variance)
# the variance became a lot smaller and this means smaller noise, which is a lot more significant

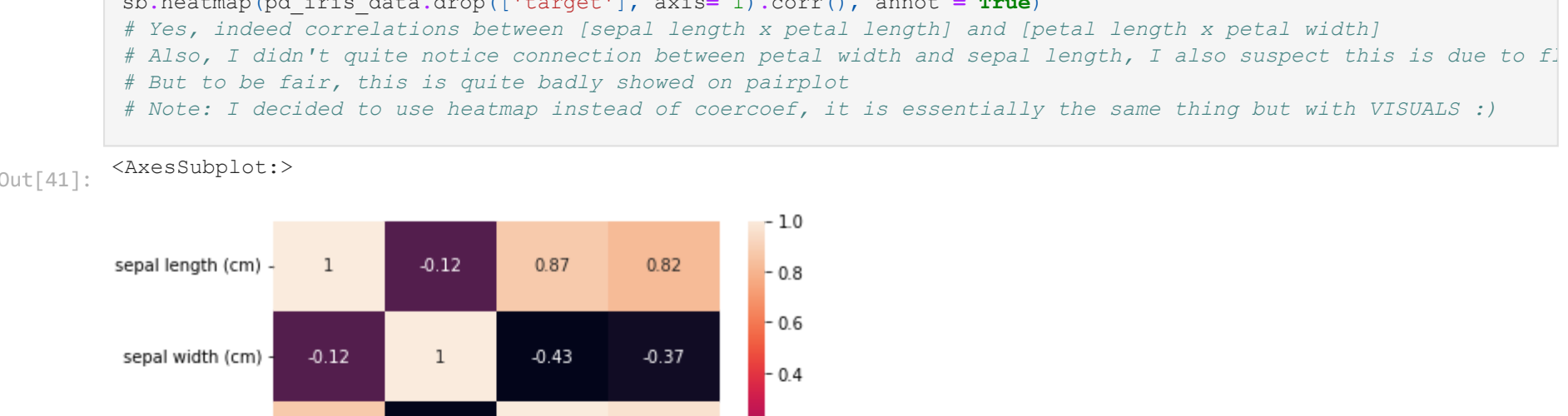
Transformed
matrix: [[0.5         0.         1.         ]
 [1.         0.5        0.33333333]
 [0.         1.         0.         ]]
mean: 0.48148148148148145
variance: 0.16941015089163236
```

```
In [39]: # D.2
# make it a pandas dataframe object
pd_iris_data = pd.DataFrame(data=np.c_[iris_dataset['data'], iris_dataset['target']],
                           columns=iris_dataset['feature_names'] + ['target'])
for n in range(3):
    print(f'iris {n} % (n, names_of_classes[n])')
    sb.pairplot(pd_iris_data, hue='target')
```

```
# Better combinations are: petal length x width
# train_X = train_X.drop(columns=[petal_width, sepal_width, sepal_length, petal_width])
# all these flowers have similar petals
# sepal length x petal length
# the bigger the flower is, the bigger are both of its parts.
# Also, it is worth mentioning that even if flowers' proportions are similar, they are not the same.
# Smaller are setosa, then comes versicolor and then virginica.
```

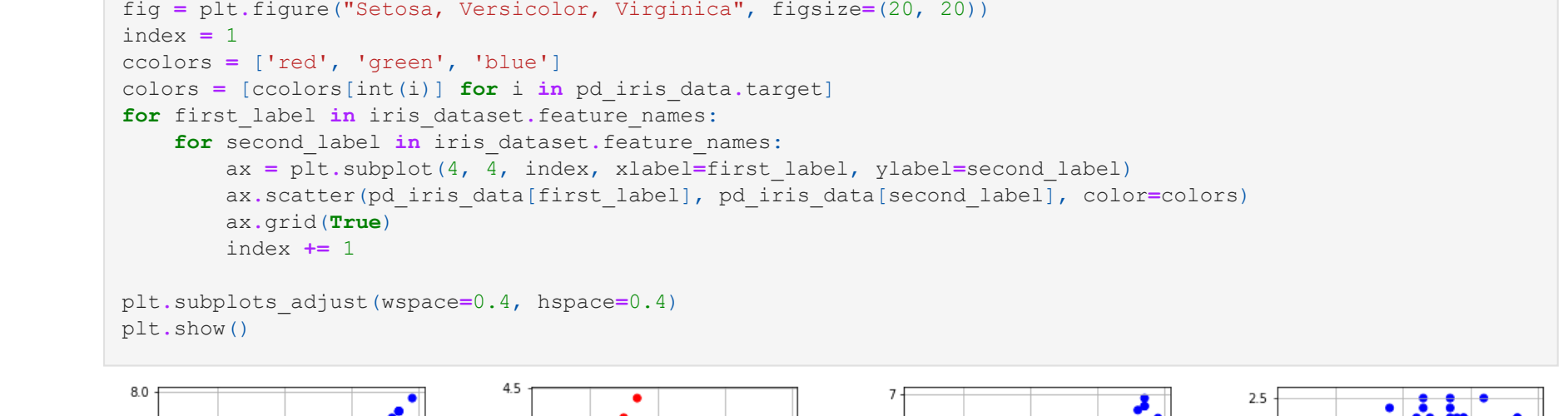
```
# I don't really get what needs to be justified here since all the results are printed and in given cases you can see the correlation (well yeah, the 'line' on the graph)

0 : setosa
1 : versicolor
2 : virginica
<seaborn.axisgrid.PairGrid at 0x15f73aafad>
```



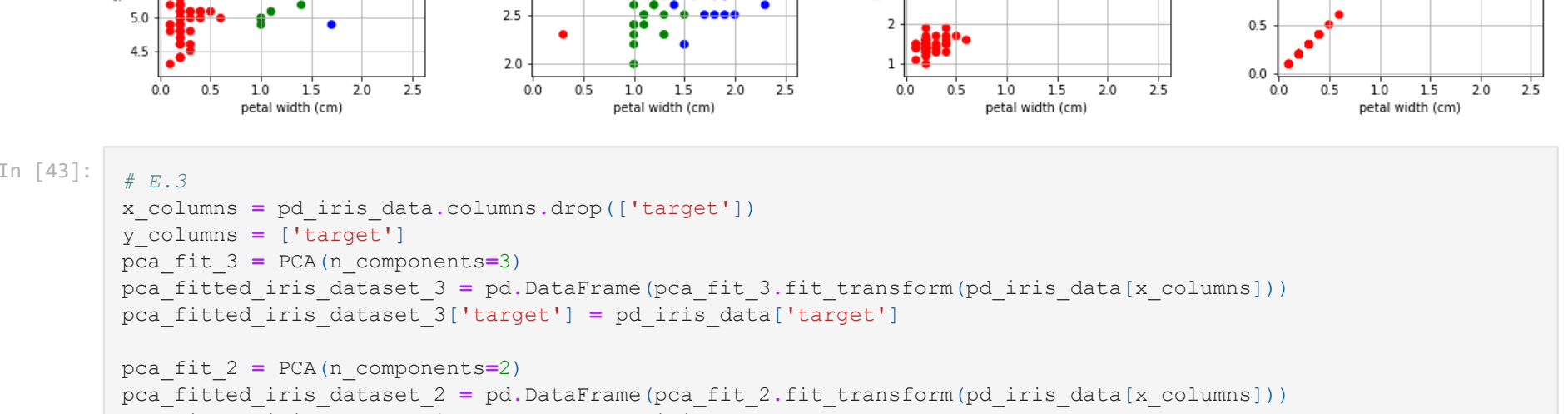
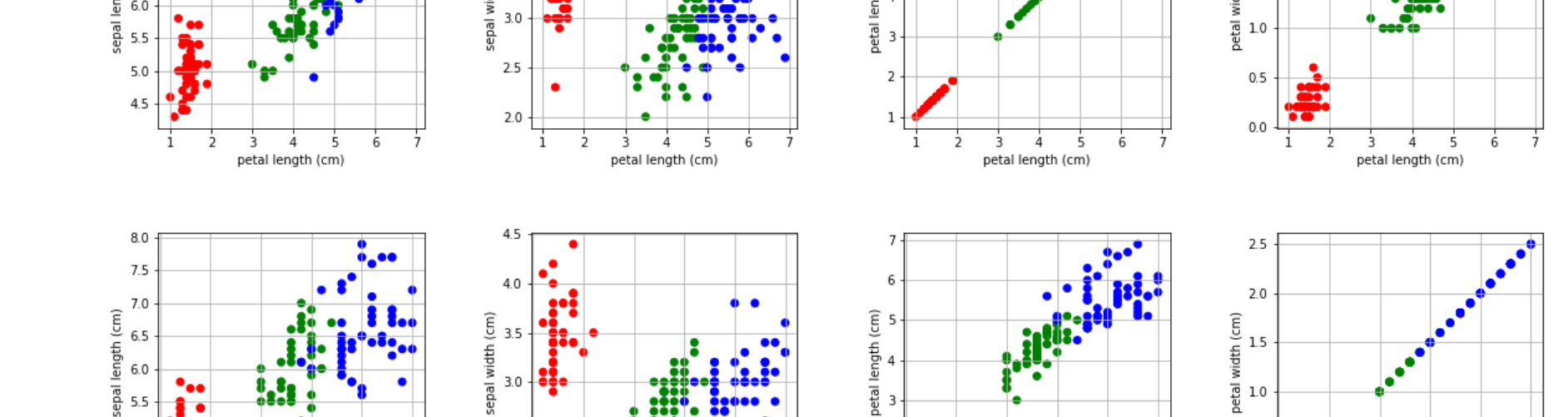
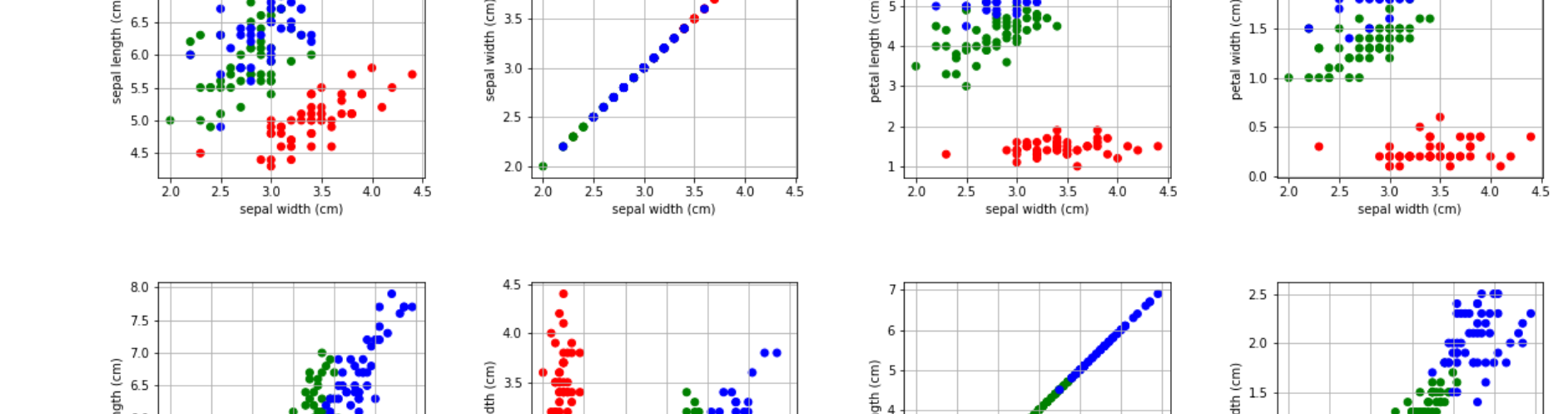
```
In [40]: for n in pd_iris_data.columns:
    print(n)
```

```
In [41]: # D.3
sb.heatmap(pd_iris_data.drop(['target'], axis=1).corr(), annot=True)
# Yes, indeed correlations between (sepal length x petal length) and (petal length x petal width)
# No, I didn't find a correlation between petal width and sepal length, I also suspect this is due to the fact that the correlation is very low.
# But to be fair, this is quite badly showed on pairplot
# Note: I decided to use heatmap instead of coercoef, it is essentially the same thing but with VISUALS :)
```



```
In [42]: # D.4
fig = plt.figure('Setosa, Versicolor, Virginica', figsize=(20, 20))
index = 1
colors = ['red', 'green', 'blue']
for first_label in range(3):
    for second_label in range(3):
        ax = plt.subplot(4, 4, index, xlabel=first_label, ylabel=second_label)
        ax.scatter(pd_iris_data[first_label], pd_iris_data[second_label], color=colors[index])
        ax.grid(True)
        index += 1

plt.subplots_adjust(wspace=0.4, hspace=0.4)
plt.show()
```



```
In [43]: # E.3
x_columns = pd_iris_data.columns.drop(['target'])
y_columns = ['target']
pca_fit_1 = PCA(n_components=3)
pca_fit_1.fit(pd_iris_data[x_columns])
pca_fit_1.transform(pd_iris_data[x_columns])
pca_fit_1.transform(pd_iris_data[0])
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